

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Fischhoff, David A
Fuchs, Roy L
Perlak, Frederick J

(ii) TITLE OF INVENTION: Insect Resistant Plants

(iii) NUMBER OF SEQUENCES: 54

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/027,998
(B) FILING DATE: 23-FEB-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Patterson, Melinda L
(B) REGISTRATION NUMBER: 33,062
(C) REFERENCE/DOCKET NUMBER: MOBT:195

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2615 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAGCGACTAT TATAATCATA CATATTTCT ATTGGAATGA TTAAGATTCC AATAGAATAG 60
TGTATAAATT ATTTATCTTG AAAGGAGGGA TGCCTAAAAA CGAAGAACAT TAAAAACATA 120
TATTTGCACC GTCTAATGGA TTTATGAAAA ATCATTAT CAGTTGAAA ATTATGTATT 180
ATGATAAGAA AGGGAGGAAG AAAAATGAAT CCGAACAAATC GAAGTGAACA TGATACAATA 240
AAAACTACTG AAAATAATGA GGTGCCAACT AACCATGTTA AATATCCTT AGCGGAAACT 300
CCAAATCCAA CACTAGAAGA TTTAAATTAT AAAGAGTTT TAAGAATGAC TGCAGATAAT 360
AATACGGAAG CACTAGATAG CTCTACAACA AAAGATGTCA TTCAAAAAGG CATTCCGTA 420
GTAGGTGATC TCCTAGGCGT AGTAGGTTTC CCGTTGGTG GAGCGCTTGT TTCGTTTAT 480
ACAAACTTT TAAATACTAT TTGGCCAAGT GAAGACCCGT GGAAGGCTTT TATGGAACAA 540
GTAGAAGCAT TGATGGATCA GAAAATAGCT GATTATGCAA AAAATAAAGC TCTTGCAGAG 600
TTACAGGGCC TTCAAAATAA TGTCGAAGAT TATGTGAGTG CATTGAGTTA ATGGCAAAAA 660
AATCCTGTGA GTTCACGAAA TCCACATAGC CAGGGCGGA TAAGAGAGCT GTTTCTCAA 720
GCAGAAAGTC ATTTTCGTA TTCAATGCCT TCGTTGCAA TTTCTGGATA CGAGGTTCTA 780
TTTCTAACAA CATATGCACA AGCTGCCAAC ACACATTTAT TTTTACTAAA AGACGCTCAA 840
ATTATGGAG AAGAATGGGG ATACGAAAAA GAAGATATTG CTGAATTAA TAAAAGACAA 900
CTAAAACCTTA CGCAAGAATA TACTGACCAT TGTGTCAAAT GGTATAATGT TGGATTAGAT 960
AAATTAAGAG GTTCATCTTA TGAATCTTGG GTAAACCTTA ACCGTTATCG CAGAGAGATG 1020
ACATTAACAG TATTAGATTT AATTGCACTA TTTCCATTGT ATGATGTTG GCTATACCA 1080
AAAGAAGTTA AAACCGAATT ACAAGAGAC GTTTAACAG ATCCAATTGT CGGAGTCAAC 1140
AACCTTAGGG GCTATGGAAC AACCTCTCT AATATAGAAA ATTATATTG AAAACCACAT 1200
CTATTTGACT ATCTGCATAG AATTCAATT CACACGCGGT TCCAACCAGG ATATTATGGA 1260
AATGACTCTT TCAATTATTG GTCCGGTAAT TATGTTCAA CTAGACCAAG CATAGGATCA 1320
AATGATATAA TCACATCTCC ATTCTATGGA AATAAATCCA GTGAACCTGT ACAAAATTAA 1380
GAATTTAATG GAGAAAAAGT CTATAGAGCC GTAGCAAATA CAAATCTTGC GGTCTGGCCG 1440
TCCGCTGTAT ATTCAAGGTGT TACAAAAGTG GAATTAGCC AATATAATGA TCAAACAGAT 1500
GAAGCAAGTA CACAAACGTA CGACTCAAAA AGAAATGTTG GCGCGGTCAAG CTGGGATTCT 1560
ATCGATCAAT TGCCTCCAGA AACAAACAGAT GAACCTCTAG AAAAGGGATA TAGCCATCAA 1620

CTCAATTATG TAATGTGCTT TTTAATGCAG GGTAGTAGAG GAACAATCCC AGTGTAACT	1680
TGGACACATA AAAGTGTAGA CTTTTTTAAC ATGATTGATT CGAAAAAAAT TACACAACCTT	1740
CCGTTAGTAA AGGCATATAA GTTACAATCT GGTGCTTCG TTGTCGCAGG TCCTAGGTTT	1800
ACAGGAGGAG ATATCATTCA ATGCACAGAA AATGGAAGTG CGGCAACTAT TTACGTTACA	1860
CCGGATGTGT CGTACTCTCA AAAATATCGA GCTAGAATTG ATTATGCTTC TACATCTCAG	1920
ATAACATTTA CACTCAGTTT AGACGGGGCA CCATTTAAC AATACTATTT CGATAAAACG	1980
ATAAATAAAG GAGACACATT AACGTATAAT TCATTTAATT TAGCAAGTTT CAGCACACCA	2040
TTCGAATTAT CAGGGAATAA CTTACAAATA GGCACACAG GATTAAGTGC TGGAGATAAA	2100
GTTTATATAG ACAAAATTGA ATTTATTCCA GTGAATTAAA TTAACTAGAA AGTAAAGAAG	2160
TAGTGACCAT CTATGATAGT AAGCAAAGGA TAAAAAAATG AGTCATAAA ATGAATAACA	2220
TAGTGTTCTT CAACTTCGC TTTTGAGG TAGATGAAGA ACACATTTC TATTTCAAA	2280
ATGAAGGAAG TTTAAATAT GTAATCATT AAAGGAAACA ATGAAAGTAG GAAATAAGTC	2340
ATTATCTATA ACAAAATAAC CATTTCATA TAGCCAGAAA TGAATTATAA TATTAATCTT	2400
TTCTAAATTG ACGTTTCTT AAACGTTCTA TAGCTCAAG ACGCTTAGAA TCATCAATAT	2460
TTGTATACAG AGCTGTTGTT TCCATCGAGT TATGTCCCAT TTGATTGCT AATAGAACAA	2520
GATCTTTATT TTCGTTATAA TGATTGGTTG CATAAGTATG GCGTAATTAA TGAGGGCTTT	2580
TCTTTCATC CAAAAGCCAA GTGTATTCT CTGTA	2615

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 644 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Thr Thr Glu			
1	5	10	15
10	15		

Asn Asn Glu Val Pro Thr Asn His Val Gln Tyr Pro Leu Ala Glu Thr		
20	25	30
30		

Pro Asn Pro Thr Leu Glu Asp Leu Asn Tyr Lys Glu Phe Leu Arg Met
35 40 45

Thr Ala Asp Asn Asn Thr Glu Ala Leu Asp Ser Ser Thr Thr Lys Asp
50 55 60

Val Ile Gln Lys Gly Ile Ser Val Val Gly Asp Leu Leu Gly Val Val
65 70 75 80

Gly Phe Pro Phe Gly Gly Ala Leu Val Ser Phe Tyr Thr Asn Phe Leu
85 90 95

Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Glu Gln
100 105 110

Val Glu Ala Leu Met Asp Gln Lys Ile Ala Asp Tyr Ala Lys Asn Lys
115 120 125

Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Val Glu Asp Tyr Val
130 135 140

Ser Ala Leu Ser Ser Trp Gln Lys Asn Pro Val Ser Ser Arg Asn Pro
145 150 155 160

His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His
165 170 175

Phe Arg Asn Ser Met Pro Ser Phe Ala Ile Ser Gly Tyr Glu Val Leu
180 185 190

Phe Leu Thr Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Phe Leu Leu
195 200 205

Lys Asp Ala Gln Ile Tyr Gly Glu Glu Trp Gly Tyr Glu Lys Glu Asp
210 215 220

Ile Ala Glu Phe Tyr Lys Arg Gln Leu Lys Leu Thr Gln Glu Tyr Thr
225 230 235 240

Asp His Cys Val Lys Trp Tyr Asn Val Gly Leu Asp Lys Leu Arg Gly
245 250 255

Ser Ser Tyr Glu Ser Trp Val Asn Phe Asn Arg Tyr Arg Arg Glu Met
260 265 270

Thr Leu Thr Val Leu Asp Leu Ile Ala Leu Phe Pro Leu Tyr Asp Val
275 280 285

Arg Leu Tyr Pro Lys Glu Val Lys Thr Glu Leu Thr Arg Asp Val Leu
290 295 300

Thr Asp Pro Ile Val Gly Val Asn Asn Leu Arg Gly Tyr Gly Thr Thr
305 310 315 320

Phe Ser Asn Ile Glu Asn Tyr Ile Arg Lys Pro His Leu Phe Asp Tyr
325 330 335

Leu His Arg Ile Gln Phe His Thr Arg Phe Gln Pro Gly Tyr Tyr Gly
340 345 350

Asn Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Ser Thr Arg Pro
355 360 365

Ser Ile Gly Ser Asn Asp Ile Ile Thr Ser Pro Phe Tyr Gly Asn Lys
370 375 380

Ser Ser Glu Pro Val Gln Asn Leu Glu Phe Asn Gly Glu Lys Val Tyr
385 390 395 400

Arg Ala Val Ala Asn Thr Asn Leu Ala Val Trp Pro Ser Ala Val Tyr
405 410 415

Ser Gly Val Thr Lys Val Glu Phe Ser Gln Tyr Asn Asp Gln Thr Asp
420 425 430

Glu Ala Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Val Gly Ala Val
435 440 445

Ser Trp Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp Glu Pro
450 455 460

Leu Glu Lys Gly Tyr Ser His Gln Leu Asn Tyr Val Met Cys Phe Leu
465 470 475 480

Met Gln Gly Ser Arg Gly Thr Ile Pro Val Leu Thr Trp Thr His Lys
485 490 495

Ser Val Asp Phe Phe Asn Met Ile Asp Ser Lys Lys Ile Thr Gln Leu
500 505 510

Pro Leu Val Lys Ala Tyr Lys Leu Gln Ser Gly Ala Ser Val Val Ala
515 520 525

Gly Pro Arg Phe Thr Gly Gly Asp Ile Ile Gln Cys Thr Glu Asn Gly
530 535 540

Ser Ala Ala Thr Ile Tyr Val Thr Pro Asp Val Ser Tyr Ser Gln Lys
545 550 555 560

Tyr Arg Ala Arg Ile His Tyr Ala Ser Thr Ser Gln Ile Thr Phe Thr
565 570 575

Leu Ser Leu Asp Gly Ala Pro Phe Asn Gln Tyr Tyr Phe Asp Lys Thr
580 585 590

Ile Asn Lys Gly Asp Thr Leu Thr Tyr Asn Ser Phe Asn Leu Ala Ser
595 600 605

Phe Ser Thr Pro Phe Glu Leu Ser Gly Asn Asn Leu Gln Ile Gly Val
610 615 620

Thr Gly Leu Ser Ala Gly Asp Lys Val Tyr Ile Asp Lys Ile Glu Phe
625 630 635 640

Ile Pro Val Asn

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Thr Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGAATCCNA ATAATCGNTC NGAACATGAT ACNATTAAAA CNACN

45

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGAACCCNA ACAACAGAAG TGAGCACGAC ACNATCAAGA CNACN

45

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGAATCCNA ATAATCGGTC CGAACATGAT ACNATAAAAA CNACN

45

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAAYCCNA AYAAYCG

17

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GARCAYGAYA CRATHAA

17

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAACAATCC CAGTGTTAG TAGGTAGCTA GCCAGATCTT TATTT

45

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAATAAAGAT CTGGCTAGCT ACCTACTAAA CACTGGGATT GTTCC

45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly Thr Ile Pro Val Phe Ser Arg Leu Ala Arg Ser Leu Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTACAGGCGG AGATTAGTAG GTAGCTAGCC AGATCTTTAT TTTC

44

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAAAATAAAG ATCTGGCTAG CTACCTACTA ATCTCCGCCT GTAA

44

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr Gly Gly Asp Val Ala Ser Gln Ile Phe Ile Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTCAGTTTAG ACAGGGCTAG TAGGTAGCTA GCCAGATCTT TATTT

45

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAATAAAGAT CTGGCTAGCT ACCTACTAGC CCCGTCTAAA CTGAG

45

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Ser Leu Asp Gly Ala Ser Arg Leu Ala Arg Ser Leu Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTTTATATAG ACAAAATTGA ATTTAGTAGG TAGCTAGCCA GATCTTTATT TT

52

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAAATAAAAGA TCTGGCTAGC TACCTACTAA ATTCAATTGTCTATATAAC

52

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Val Tyr Ile Asp Lys Ile Glu Phe Ser Arg Leu Ala Arg Ser Leu Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TATAAAGAGT TTTTAAGAAT AACTGCAGAT AATAATA

37

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TATTATTATC TGCAGTTATT CTTAAAAACT CTTTATA

37

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr Lys Glu Phe Leu Arg Ile Thr Ala Asp Asn Asn Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCATGGATGC AGATAATAAT ACGGAAGCAC TAGATAGCTC T

41

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGAGCTATCT AGTGCTTCCG TATTATTATC TGCATCCATG G

41

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Asp Ala Asp Asn Asn Thr Glu Ala Leu Asp Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCATGCTAGG AGTAGTAGGT TTCCCGTTG TGGAGCGCTT G

41

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAAGCGCTCC ACAAACGGGA AACCTACTAC TCCTAGCATG G

41

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Leu Gly Val Val Gly Phe Pro Phe Val Glu Arg Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCATGGCAAT TTGGCCAAGT GAAGAC

26

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCTTCACCTT GGCCAAATTG CCATGG

26

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ala Ile Trp Pro Ser Glu Asp
1 5

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AAGCTTGCAT GCCTGCAGGT CCGATGTGAG ACTTTCAAC AAAGGGTAAT ATCCGGAAAC	60
CTCCTCGGAT TCCATTGCCC AGCTATCTGT CACTTATTG TGAAGATAGT GGAAAAGGAA	120
GGTGGCTCCT ACAAAATGCCA TCATTGCGAT AAAGGAAAGG CCATCGTTGA AGATGCCTCT	180
GCCGACAGTG GTCCCAAAGA TGGACCCCCA CCCACGAGGA GCATCGTGGAA AAAAGAAGAC	240
GTTCCAACCA CGTCTTCAAA GCAAGTGGAT TGATGTGATG GTCCGATGTG AGACTTTCA	300
ACAAAGGGTA ATATCCGGAA ACCTCCTCGG ATTCCATTGC CCAGCTATCT GTCACTTTAT	360
TGTGAAGATA GTGGAAAAGG AAGGTGGCTC CTACAAATGC CATCATTGCG ATAAAGGAAA	420
GGCCATCGTT GAAGATGCCT CTGCCGACAG TGGTCCAAA GATGGACCCCC CACCCACGAG	480
GAGCATCGTG GAAAAAGAAG ACGTTCCAAC CACGTCTTCA AAGCAAGTGG ATTGATGTGA	540
TATCTCCACT GACGTAAGGG ATGACGCACA ATCCCACTAT CCTTCGCAAG ACCCTTCCTC	600
TATATAAGGA AGTCATTTC ATTTGGAGAG GACACGCTGA CAAGCTGACT CTAGCAGATC	660
T	661

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Xaa Pro Xaa Thr Arg Ala Leu Asp Asp Thr Ile Lys Lys Asp Val
1 5 10 15
Ile Gln Lys

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGAACATGGT TAGTTGG 17

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TAGGTGATCT CTAGGCG 17

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGAACAAACCT TCTCTAATAT

20

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATGAAYCCNA AYAAYCG

17

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GARCAYGAYA CYATHAA

17

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GATTGTTCGG ATCCATGGTT CTTCCCTCCCT

30

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TAGTAGGTAG CTAGCCA

17

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCTGGCTA GCTACCTACT A

21

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGTATTATTA TCTGCATCCA TGGTTCTTCC TCCCT

35

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATTATTATCT GCAGTTATTC TTAAAAACTC TTTAT

35

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCACTTGGCC AAATTGCCAT GGTATTTAAA AAGTTTGT

38

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATGATAAGAA AGGGAGGAAG AAAAATGAAT CCGAACAAATC GAAAGTGAACA TGATACAATA

60

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CGGATTCATT TTAGATCTTC CTCCCTT

27

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTTTATATAG ACAAAATTGA ATTTATTCCA GTGAATTAAA TTAACTAGAA AGTAAAGAAG

60

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Val Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTTTCTAGTT AAAGATCTTT AATTCACTG

29

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CCAAATCCAA CACTAGAAGA TTTAAATTAT AAAGAGTTTT TAAGAATGAC TGCAGATAAT

60

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro Asn Pro Thr Leu Glu Asp Leu Asn Tyr Lys Glu Phe Leu Arg Met
1 5 10 15

Thr Ala Asp Asn
20

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATCTGCAGTC ATTGTAGATC TCTCTTATA ATTT

34